

D. Srivastava

#11 1653  
7/13/99

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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/962,560A**

DATE: 07/13/1999  
TIME: 15:32:26

### INPUT SET: S32531.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

## SEQUENCE LISTING

(1) General Information:

5 (i) APPLICANT: Hilton, Douglas J.  
6 Alexander, Warren S.  
7 Viney, Elizabeth M.  
8 Willson, Tracy A.  
9 Richardson, Rachael T.  
10 Starr, Robyn  
11 Nicholson, Sandra E.  
12 Metcalf, Donald  
13 Nicola, Nicos A.

ENTERED

15 (ii) TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS

17 (iii) NUMBER OF SEQUENCES: 50

19 (iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Scully, Scott, Murphy & Presser  
21 (B) STREET: 400 Garden City Plaza  
22 (C) CITY: Garden City, New York  
23 (D) STATE: New York  
24 (E) COUNTRY: U.S.A.  
25 (F) ZIP: 11530

27 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

33 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/962,560  
(B) FILING DATE: 31-OCT-1997

37 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/AU97/00729  
(B) FILING DATE: 31-OCT-1997

41 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: P05117  
(B) FILING DATE: 14-FEB-1997

45 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO 3384

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PATENT APPLICATION US/08/962,560ADATE: 07/13/1999  
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47 (B) FILING DATE: 01-NOV-1996  
48  
49 (viii) ATTORNEY/AGENT INFORMATION:  
50 (A) NAME: DiGiglio, Frank S.  
51 (B) REGISTRATION NO: 31,346  
52 (C) REFERENCE/DOCKET NUMBER: 10976  
53  
54 (ix) TELECOMMUNICATION INFORMATION:  
55 (A) TELEPHONE: (516) 742-4343  
56 (B) TELEFAX: (516) 742-4366  
57 (C) TELEX:  
58  
59 (2) INFORMATION FOR SEQ ID NO:1:  
60  
61 (i) SEQUENCE CHARACTERISTICS:  
62 (A) LENGTH: 20 base pairs  
63 (B) TYPE: nucleic acid  
64 (C) STRANDEDNESS: single  
65 (D) TOPOLOGY: linear  
66  
67 (ii) MOLECULE TYPE: DNA  
68  
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
70  
71 CACGCCGCC ACAGTGAAGGC 20  
72  
73 (2) INFORMATION FOR SEQ ID NO:2:  
74  
75 (i) SEQUENCE CHARACTERISTICS:  
76 (A) LENGTH: 20 base pairs  
77 (B) TYPE: nucleic acid  
78 (C) STRANDEDNESS: single  
79 (D) TOPOLOGY: linear  
80  
81 (ii) MOLECULE TYPE: DNA  
82  
83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
84  
85 TTTCGCCAATG ACAAGACGCT 20  
86  
87 (2) INFORMATION FOR SEQ ID NO:3:  
88  
89 (i) SEQUENCE CHARACTERISTICS:  
90 (A) LENGTH: 1235 base pairs  
91 (B) TYPE: nucleic acid  
92 (C) STRANDEDNESS: single  
93 (D) TOPOLOGY: linear  
94  
95 (ii) MOLECULE TYPE: DNA  
96  
97 (ix) FEATURE:  
98 (A) NAME/KEY: CDS  
99 (B) LOCATION: 161..799

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100  
 101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
 102  
 103 CGAGGCTCAA GCTCCGGCG GATTCTGCGT GCCGCTCTCG CTCCCTGGGG TCTGTTGCC 60  
 104  
 105 GGCCTGTGCC ACCCGGACGC CCGGCTCACT GCCTCTGTCT CCCCCATCAG CGCAGCCCCG 120  
 106  
 107 GACGCTATGG CCCACCCCTC CAGCTGGCCC CTCGAGTAGG 160  
 108  
 109 ATG GTA GCA CGC AAC CAG GTG GCA GCC GAC AAT GCG ATC TCC CCG GCA 208  
 110 Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala  
 111 1 5 10 15  
 112  
 113 GCA GAG CCC CGA CGG CGG TCA GAG CCC TCC TCG TCC TCG TCT TCG TCC 256  
 114 Ala Glu Pro Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser  
 115 20 25 30  
 116  
 117 TCG CCA GCG GCC CCC GTG CGT CCC CGG CCC TGC CCG GCG GTC CCA GCC 304  
 118 Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala  
 119 35 40 45  
 120  
 121 CCA GCC CCT GGC GAC ACT CAC TTC CGC ACC TTC CGC TCC CAC TCC GAT 352  
 122 Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp  
 123 50 55 60  
 124  
 125 TAC CGG CGC ATC ACG CGG ACC AGC GCG CTC CTG GAC GCC TGC GGC TTC 400  
 126 Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe  
 127 65 70 75 80  
 128  
 129 TAT TGG GGA CCC CTG AGC GTG CAC GGG GCG CAC GAG CGG CTG CGT GCC 448  
 130 Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala  
 131 85 90 95  
 132  
 133 GAG CCC GTG GGC ACC TTC TTG GTG CGC GAC AGT CGT CAA CGG AAC TGC 496  
 134 Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys  
 135 100 105 110  
 136  
 137 TTC TTC GCG CTC AGC GTG AAG ATG GCT TCG GGC CCC ACG AGC ATC CGC 544  
 138 Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg  
 139 115 120 125  
 140  
 141 GTG CAC TTC CAG GCC GGC CGC TTC CAC TTG GAC GGC AGC CGC GAG ACC 592  
 142 Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr  
 143 130 135 140  
 144  
 145 TTC GAC TGC CTT TTC GAG CTG CTG GAG CAC TAC GTG GCG GCG CCG CGC 640  
 146 Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg  
 147 145 150 155 160  
 148  
 149 CGC ATG TTG GGG GCC CCG CTG CGC CAG CGC CGC GTG CGG CCG CTG CAG 688  
 150 Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln  
 151 165 170 175  
 152

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PATENT APPLICATION US/08/962,560ADATE: 07/13/1999  
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153 GAG CTG TGT CGC CAG CGC ATC GTG GCC GCC GTG GGT CGC GAG AAC CTG 736  
 154 Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu  
 155 180 185 190  
 156 GCG CGC ATC CCT CTT AAC CCG GTA CTC CGT GAC TAC CTG AGT TCC TTC 784  
 157 Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe  
 158 195 200 205  
 159  
 160 CCC TTC CAG ATC TGA CCGGCTG CCGCTGTGCC GCAGCATTAA GTGGGGCGC 836  
 161 Pro Phe Gln Ile  
 162 210  
 163  
 164 CTTATTATTT CTTATTATTA ATTATTATTA TTTTCTGGA ACCACGTGGG AGCCCTCCCC 896  
 165  
 166 GCCTGGGTGG GAGGGAGTGG TTGTGGAGGG TGAGATGCCT CCCACTTCTG GCTGGAGACC 956  
 167  
 168 TCATCCCACC TCTCAGGGGT GGGGGTGCTC CCCTCCTGGT GCTCCCTCCG GGTCCCCCCT 1016  
 169  
 170 GGTTGTAGCA GCTTGTGTCT GGGGCCAGGA CCTGAATTCC ACTCCTACCT CTCCATGTTT 1076  
 171  
 172 ACATATTCCC AGTATCTTTG CACAAACCAG GGGTCGGGA GGGTCTCTGG CTTCATTTTT 1136  
 173  
 174 CTGCTGTGCA GAATATCCTA TTTTATATTT TTACAGCCAG TTTAGGTAAT AAACTTTATT 1196  
 175  
 176 ATGAAAGTTT TTTTTAAAAA GAAAAAAA AAAAAAAA 1235  
 177  
 178 (2) INFORMATION FOR SEQ ID NO:4:  
 179  
 180 (i) SEQUENCE CHARACTERISTICS:  
 181 (A) LENGTH: 212 amino acids  
 182 (B) TYPE: amino acid  
 183 (D) TOPOLOGY: linear  
 184  
 185 (ii) MOLECULE TYPE: protein  
 186  
 187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
 188  
 189 Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala  
 190 1 5 10 15  
 191  
 192 Ala Glu Pro Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser  
 193 20 25 30  
 194  
 195 Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala  
 196 35 40 45  
 197  
 198 Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp  
 199 50 55 60  
 200  
 201 Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe  
 202 65 70 75 80  
 203  
 204 Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala  
 205 85 90 95

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206 Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys  
207 100 105 110  
208  
209 Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg  
210 115 120 125  
211  
212 Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr  
213 130 135 140  
214  
215 Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg  
216 145 150 155 160  
217  
218 Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln  
219 165 170 175  
220  
221 Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu  
222 180 185 190  
223  
224 Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe  
225 195 200 205  
226  
227 Pro Phe Gln Ile  
228 210  
229  
230  
231 (2) INFORMATION FOR SEQ ID NO:5:  
232  
233 (i) SEQUENCE CHARACTERISTICS:  
234 (A) LENGTH: 1121 base pairs  
235 (B) TYPE: nucleic acid  
236 (C) STRANDEDNESS: single  
237 (D) TOPOLOGY: linear  
238  
239 (ii) MOLECULE TYPE: DNA  
240  
241 (ix) FEATURE:  
242 (A) NAME/KEY: CDS  
243 (B) LOCATION: 223..819  
244  
245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
246  
247 GCGATCTGTG GGTGACAGTG TCTGCGAGAG ACTTTGCCAC ACCATTCTGC CGGAATTTGG 60  
248  
249 AGAAAAAGAA CCAGCCGCTT CCAGTCCCCT CCCCCCTCCGC CACCATTCG GACACCCCTGC 120  
250  
251 ACACCTCTCGT TTTGGGGTAC CCTGTGACTT CCAGGCAGCA CGCGAGGTCC ACTGGCCCCA 180  
252  
253 GCTCGGGCGA CCAGCTGTCT GGGACGTGTT GACTCATCTC CC ATG ACC CTG CGG 234  
254 Met Thr Leu Arg  
255 1  
256  
257  
258 TGC CTG GAG CCC TCC GGG AAT GGA GCG GAC AGG ACG CGG AGC CAG TGG 282

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**SEQUENCE VERIFICATION REPORT**  
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